

WHAT IS CLAIMED IS:

1. A method for generating an siRNA expression library for selective post-transcriptional silencing of genes encoding a family of proteins, the method comprising:
 - i. identifying a consensus sequence for the family of proteins; and,
 - ii. generating an siRNA expression library whose members encode siRNA molecules that target at least all mRNA encoding all known members of the family of proteins.
2. The method of claim 1, wherein the consensus sequence comprises between 15 to 30 nucleotides.
3. The method of claim 1, wherein the consensus sequence comprises between 18 to 24 nucleotides.
4. The method of claim 1, wherein the library comprises between 50 and one million unique members.
5. The method of claim 1, wherein the library comprises between 20,000 and 100,000 unique members.
6. The method of claim 1, wherein the family of proteins is selected from the group consisting of: G protein coupled receptors, ion channels, receptor tyrosine kinases, non-receptor tyrosine kinases, nuclear hormone receptors, GTPases, ATPases, serine/threonine kinases, proteases, matrix metalloproteinases (MMPs), GTPase-activating proteins (GAPs) and E3 ubiquitin ligases.
7. The method according to claim 1 wherein the step of identifying a consensus sequence comprises identifying at least one signature motif for the family of proteins.
8. The method according to claim 1 wherein the step of identifying a consensus sequence comprises identifying two or more variants of a signature motif for the family of proteins.

9. An siRNA expression library for selective post-transcriptional silencing of genes encoding a family of proteins, wherein members of the library encode siRNA molecules that are of between 15 to 30 nucleotides in length and target at least all mRNA encoding all known members of the family of proteins, and wherein the library comprises up to one million unique members.

10. The library of claim 9, wherein the library comprises up to 100,000 unique members.

11. The library of claim 9, wherein the family of proteins is selected from the group consisting of: G protein coupled receptors, ion channels, receptor tyrosine kinases, non-receptor tyrosine kinases, nuclear hormone receptors, GTPases, ATPases, serine/threonine kinases, proteases, matrix metalloproteinases (MMPs), GTPase-activating proteins (GAPs) and E3 ubiquitin ligases.

12. The library of claim 9, wherein the siRNA molecules are between 18 to 24 nucleotides in length.